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SEQUENCE LISTING

<110> Osaka Industrial Promotion Organization
National Institute of Radiological Sciences
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<120> Development of Mammalian Genome Modification Technique
using Retrotransposon

<130> OT004US

<140> PCT/JP2004/017307
<141> 2004-11-19

<150> JP 2003-393175
<151> 2003-11-21

<160> 40

<170> PatentIn version 3.2

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<213> Mus musculus

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<223> IAP sequence actually used in the Examples for exemplification

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Gly Asp Asn Val Asp Ile Ser Thr Pro Asn Asp Gly Asp Val				
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taatgctcaa gtattctcct gcttttttac cactaactag gaactgggtt tggccttaat				5914
tcagacagcc ttggctctgt ctggacaggt ccagatgact gacaccatta acactttgtc				5974
agcctcagtg actacagtca tagatgaaca ggcctcagct aatgtcaaga tacagagagg				6034
tctcatgctg gttaatcaac tcatagatct tgtccagaaa caactggatg tattatgaca				6094
aataactcag cagggatgtg aacaaaagtt tccgggattg tgtgttattt ccattcagta				6154
tgttaaattt actaggacag ctaatttgtc aaaaagtctt tttcagtata tgttacagaa				6214
ttggatggct gaatttgaat agatccttcg agaattgaga cttcagggtca actccacgcg				6274
cttggacctg tcgctgacca aaagattacc caattggatc tcctcagcat tttctttctt				6334
taaaaaattg ggtgggatta atattatttg gagatacact ttgctgtgga ttagtggtgc				6394
ttctttgatt ggtctgtaag cttaaggccc aaactaagag agacaagggtg gttattgccc				6454
aggcgcttgc aggactagaa catggagctt cccctgatat atctatgctt aagcaatagg				6514
tcgctggcca ctcagctctt atatctcacg aggctagtct cattgcacga gatagagtga				6574
gtgtgcttca gcagccccgag agagttgcaa ggctaagcac tgcagtagaa gggctctgcg				6634
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tatctccact ctcattaata tgggtggcct atttgctctt attaaaagaa aaagggggaa				6874
ctgtgggaag ccgccccac attcgccgtc acaagatggc gctgacatcc tgtgttctaa				6934
gttggtaaac aaataatctg cgcattgagcc aagggtattt acgactactt gtactctgtt				6994
tttcccgtga acgtcagctc ggccatgggc tgcagccaat cagggagtga tgcgccctag				7054
gcaatggttg ttctctttta aatagaaggg gtttcgtttt tctcgctctc ttgcttcttg				7114
ctctctcttg ctccctctc ttgcttcttg ctctctcttg ctccctctc ttgcttcttg				7174
ctctctcttg ctccctctc ttgcttcttg ctctctcttg ctctctgctc tcttttcctg				7234
aagatgtaag aataaagctt tgcgcagaa gattctgggc tgtggtgttc ttcctggccg				7294

gtcgtgagaa cgcgtcgaat aaca

7318

<210> 2

<211> 586

<212> PRT

<213> Mus musculus

<220>

<223> IAP sequence amino acid sequence (gag #1)

<400> 2

Met	Asn	Ser	Glu	Leu	Phe	Ser	Trp	Gly	Thr	Arg	Val	Pro	Val	Ser	Met
1				5				10						15	

Phe	Gly	Leu	Glu	Phe	Phe	Leu	Val	Leu	Gly	Ala	Leu	Leu	Phe	Leu	Phe
		20						25					30		

Thr	Cys	Tyr	Ile	Val	Val	Lys	Ala	Gly	Leu	Lys	Ile	Leu	Asp	Glu	Ile
	35					40						45			

Gln	Gly	Ser	Leu	Ser	Glu	Val	Lys	Arg	Gly	Glu	Arg	Val	Gly	Ala	Arg
	50					55					60				

Arg	Asn	Gly	Lys	Tyr	Thr	Gly	Leu	Ser	Lys	Gly	Leu	Glu	Pro	Glu	Glu
65					70					75					80

Lys	Leu	Arg	Leu	Gly	Arg	Asn	Thr	Trp	Arg	Glu	Ile	Arg	Arg	Lys	Arg
			85					90						95	

Gly	Lys	Arg	Glu	Lys	Lys	Lys	Asp	Arg	Leu	Ala	Glu	Val	Ser	Arg	Arg
			100					105						110	

Tyr	Ser	Ser	Leu	Asp	Glu	Leu	Arg	Lys	Pro	Ala	Leu	Ser	Ser	Ser	Glu
		115					120					125			

Ala	Ser	Glu	Glu	Ser	Ser	Ser	Glu	Glu	Thr	Asp	Trp	Glu	Glu	Glu	Ala
	130					135					140				

Ala	His	Tyr	Gln	Pro	Ala	Asn	Trp	Ser	Arg	Lys	Lys	Pro	Lys	Ala	Ala
145					150					155					160

Gly	Glu	Ser	Gln	Arg	Thr	Val	Gln	Pro	Pro	Gly	Ser	Arg	Phe	Gln	Gly
			165						170					175	

Pro	Pro	Tyr	Ala	Glu	Pro	Pro	Pro	Cys	Val	Val	Arg	Gln	Gln	Cys	Ala
			180					185					190		

Glu Arg Gln Cys Ala Glu Arg Cys Ala Glu Arg Gln Cys Ala Asp Arg
195 200 205

Cys Ala Glu Arg Gln Cys Ala Glu Arg Gln Cys Ala Asp Ser Phe Ile
210 215 220

Pro Arg Glu Glu Gln Lys Lys Ile Glu Gln Ala Phe Pro Val Phe Glu
225 230 235 240

Gly Ala Glu Gly Gly Arg Val His Ala Pro Val Glu Tyr Val Gln Ile
245 250 255

Lys Glu Ile Ala Glu Ser Val Arg Lys Tyr Gly Thr Asn Ala Asn Phe
260 265 270

Thr Leu Val Gln Leu Asp Arg Leu Ala Gly Met Ala Leu Thr Pro Ala
275 280 285

Asp Trp Gln Thr Val Val Lys Ala Ala Leu Pro Ser Met Gly Lys Tyr
290 295 300

Met Glu Trp Lys Ala Leu Trp His Glu Ala Ala Gln Ala Gln Ala Arg
305 310 315 320

Ala Asn Ala Ala Ala Leu Thr Pro Glu Gln Arg Asp Trp Thr Phe Asp
325 330 335

Leu Leu Thr Gly Gln Gly Ala Tyr Ser Ala Asp Gln Thr Asn Tyr His
340 345 350

Trp Gly Ala Tyr Ala Gln Ile Ser Ser Thr Ala Ile Arg Ala Trp Lys
355 360 365

Ala Leu Ser Arg Ala Gly Glu Thr Thr Gly Gln Leu Thr Lys Ile Ile
370 375 380

Gln Gly Pro Gln Glu Ser Phe Ser Asp Phe Val Ala Arg Met Thr Glu
385 390 395 400

Ala Ala Glu Arg Ile Phe Gly Glu Ser Glu Gln Ala Ala Pro Leu Ile
405 410 415

Glu Gln Leu Ile Tyr Glu Gln Ala Thr Lys Glu Cys Arg Ala Ala Ile
420 425 430

Ala Pro Arg Lys Asn Lys Gly Leu Gln Asp Trp Leu Arg Val Cys Arg
435 440 445

Glu Leu Gly Gly Pro Leu Ser Asn Ala Gly Leu Ala Ala Ala Ile Leu
450 455 460

Gln Ser Gln Asn Arg Ser Met Gly Arg Asn Asp Gln Arg Thr Cys Phe
465 470 475 480

Asn Cys Gly Lys Pro Gly His Phe Lys Lys Asp Cys Arg Ala Pro Asp
485 490 495

Lys Gln Gly Gly Thr Leu Thr Leu Cys Ser Lys Cys Gly Lys Gly Tyr
500 505 510

His Arg Ala Asp Gln Cys Arg Ser Val Arg Asp Ile Lys Gly Arg Ile
515 520 525

Leu Pro Pro Pro Asp Ser Gln Ser Ala Asp Val Pro Lys Asn Gly Ser
530 535 540

Pro Gly Pro Arg Ser Gln Gly Pro Gln Arg Tyr Gly Asn Arg Phe Val
545 550 555 560

Arg Thr Gln Glu Ala Val Arg Glu Thr Thr Gln Glu Asp Pro Gln Gly
565 570 575

Trp Thr Cys Val Pro Pro Pro Thr Ser Tyr
580 585

<210> 3

<211> 258

<212> PRT

<213> Mus musculus

<220>

<223> IAP sequence amino acid sequence (gag #2)

<400> 3

Met Pro Gln Met Ser Ile Gln Pro Val Pro Val Glu Pro Ile Pro Ser
1 5 10 15

Leu Pro Pro Gly Thr Met Gly Leu Ile Leu Gly Arg Gly Ser Leu Thr
20 25 30

Leu Gln Gly Leu Val Val His Pro Gly Ile Met Asp Cys Gln His Ser
35 40 45

Pro Glu Ile Gln Val Leu Cys Ser Ser Pro Lys Gly Val Phe Ser Ile
50 55 60

Ser Lys Gly Asp Arg Ile Ala Gln Leu Leu Leu Leu Pro Asp Asn Thr
65 70 75 80

Arg Glu Lys Ser Ala Gly Pro Glu Ile Lys Lys Met Gly Ser Ser Gly
85 90 95

Asn Asp Ser Ala Tyr Leu Val Val Ser Leu Asn Asp Arg Pro Lys Leu
100 105 110

Arg Leu Lys Ile Asn Gly Lys Glu Phe Glu Gly Ile Leu Asp Thr Gly
115 120 125

Ala Asp Lys Ser Ile Ile Ser Thr His Trp Trp Pro Lys Ala Trp Pro
130 135 140

Thr Thr Glu Ser Ser His Ser Leu Gln Gly Leu Gly Tyr Gln Ser Cys
145 150 155 160

Pro Thr Ile Ser Ser Val Ala Leu Thr Trp Glu Ser Ser Glu Gly Gln
165 170 175

Gln Gly Lys Phe Ile Pro Tyr Val Leu Pro Leu Pro Val Asn Leu Trp
180 185 190

Gly Arg Asp Ile Met Gln His Leu Gly Leu Ile Leu Ser Asn Glu Asn
195 200 205

Ala Pro Ser Gly Gly Tyr Ser Ala Lys Ala Lys Asn Ile Met Ala Lys
210 215 220

Met Gly Tyr Lys Glu Gly Lys Gly Leu Gly His Gln Glu Gln Gly Arg
225 230 235 240

Ile Glu Pro Ile Ser Pro Asn Gly Asn Gln Asp Arg Gln Gly Leu Gly
245 250 255

Phe Pro

<210> 4
<211> 805
<212> PRT
<213> Mus musculus

<220>

<223> IAP sequence amino acid sequence (pol)

<400> 4

Met Asn Leu Phe Gly Pro Val Gln Arg Gly Leu Pro Val Leu Ser Ala
1 5 10 15

Leu Pro Arg Gly Trp Asn Leu Ile Ile Ile Asp Ile Lys Asp Cys Phe
20 25 30

Phe Ser Ile Pro Leu Cys Pro Arg Asp Arg Pro Arg Phe Ala Phe Thr
35 40 45

Ile Pro Ser Ile Asn His Met Glu Pro Asp Lys Arg Tyr Gln Trp Lys
50 55 60

Val Leu Pro Gln Gly Met Ser Asn Ser Pro Thr Met Cys Gln Leu Tyr
65 70 75 80

Val Gln Glu Ala Leu Leu Pro Val Arg Glu Gln Phe Pro Ser Leu Ile
85 90 95

Leu Leu Leu Tyr Met Asp Asp Ile Leu Leu Cys His Lys Asp Leu Thr
100 105 110

Met Leu Gln Lys Ala Tyr Pro Phe Leu Leu Lys Thr Leu Ser Gln Trp
115 120 125

Gly Leu Gln Ile Ala Thr Glu Lys Val Gln Ile Ser Asp Thr Gly Gln
130 135 140

Phe Leu Gly Ser Val Val Ser Pro Asp Lys Ile Val Pro Gln Lys Val
145 150 155 160

Glu Ile Arg Arg Asp His Leu His Thr Leu Asn Asp Phe Gln Lys Leu
165 170 175

Leu Gly Asp Ile Asn Trp Leu Arg Pro Phe Leu Lys Ile Pro Ser Ala
180 185 190

Glu Leu Arg Pro Leu Phe Ser Ile Leu Glu Gly Asp Pro His Ile Ser
195 200 205

Ser Pro Arg Thr Leu Thr Leu Ala Ala Asn Gln Ala Leu Gln Lys Val
210 215 220

Glu Lys Ala Leu Gln Asn Ala Gln Leu Gln Arg Ile Glu Asp Ser Gln
 225 230 235 240

Pro Phe Ser Leu Cys Val Phe Lys Thr Ala Gln Leu Pro Thr Ala Val
 245 250 255

Leu Trp Gln Asn Gly Pro Leu Leu Trp Ile His Pro Asn Val Ser Pro
 260 265 270

Ala Lys Ile Ile Asp Trp Tyr Pro Asp Ala Ile Ala Gln Leu Ala Leu
 275 280 285

Lys Gly Leu Lys Ala Ala Ile Thr His Phe Gly Gln Ser Pro Tyr Leu
 290 295 300

Leu Ile Val Pro Tyr Thr Ala Ala Gln Val Gln Thr Leu Ala Ala Ala
 305 310 315 320

Ser Asn Asp Trp Ala Val Leu Val Thr Ser Phe Ser Gly Lys Ile Asp
 325 330 335

Asn His Tyr Pro Lys His Pro Ile Leu Gln Phe Ala Gln Asn Gln Ser
 340 345 350

Val Val Phe Pro Gln Ile Thr Val Arg Asn Pro Leu Lys Asn Gly Ile
 355 360 365

Val Val Tyr Thr Asp Gly Ser Lys Thr Gly Ile Gly Ala Tyr Val Ala
 370 375 380

Asn Gly Lys Val Val Ser Lys Gln Tyr Asn Glu Asn Ser Pro Gln Val
 385 390 395 400

Val Glu Cys Leu Val Val Leu Glu Val Leu Lys Thr Phe Leu Lys Pro
 405 410 415

Leu Asn Ile Val Ser Asp Ser Cys Tyr Val Val Asn Ala Val Asn Leu
 420 425 430

Leu Glu Val Ala Gly Val Ile Lys Pro Ser Ser Arg Val Ala Asn Ile
 435 440 445

Phe Gln Gln Ile Gln Leu Val Leu Leu Ser Arg Arg Ser Pro Val Tyr
 450 455 460

Ile Thr His Val Arg Ala His Ser Gly Leu Pro Gly Pro Met Ala Leu
465 470 475 480

Gly Asn Asp Leu Ala Asp Lys Ala Thr Lys Val Val Ala Ala Ala Leu
485 490 495

Ser Ser Pro Val Glu Ala Ala Arg Asn Phe His Asn Asn Phe His Val
500 505 510

Thr Ala Glu Thr Leu Arg Ser Arg Phe Ser Leu Thr Arg Lys Glu Ala
515 520 525

Arg Asp Ile Val Thr Gln Cys Gln Ser Cys Cys Glu Phe Leu Pro Val
530 535 540

Pro His Val Gly Ile Asn Pro Arg Gly Ile Arg Pro Leu Gln Val Trp
545 550 555 560

Gln Met Asp Val Thr His Val Ser Ser Phe Gly Lys Leu Gln Tyr Leu
565 570 575

His Val Ser Ile Asp Thr Cys Ser Gly Ile Met Phe Ala Ser Pro Leu
580 585 590

Thr Gly Glu Lys Ala Ser His Val Ile Gln His Cys Leu Glu Ala Trp
595 600 605

Ser Ala Trp Gly Lys Pro Arg Leu Leu Lys Thr Asp Asn Gly Pro Ala
610 615 620

Tyr Thr Ser Gln Lys Phe Gln Gln Phe Cys Arg Gln Met Asp Val Thr
625 630 635 640

His Leu Thr Gly Leu Pro Tyr Asn Pro Gln Gly Gln Gly Ile Val Glu
645 650 655

Arg Ala His Arg Thr Leu Lys Ala Tyr Leu Ile Lys Gln Lys Arg Gly
660 665 670

Thr Phe Glu Glu Thr Val Pro Arg Ala Pro Arg Val Ser Val Ser Leu
675 680 685

Ala Leu Phe Thr Leu Asn Phe Leu Asn Ile Asp Ala His Gly His Thr
690 695 700

Ala Ala Glu Arg His Cys Ser Glu Pro Asp Arg Pro Asn Glu Met Val

705 710 715 720

Lys Trp Lys Asn Val Leu Asp Asn Lys Trp Tyr Gly Pro Asp Pro Ile
725 730 735

Leu Ile Arg Ser Arg Gly Ala Ile Cys Val Phe Pro Gln Asn Glu Asp
740 745 750

Asn Pro Phe Trp Val Pro Glu Arg Leu Thr Arg Lys Ile Gln Thr Asp
755 760 765

Gln Gly Asn Thr Asn Val Pro Arg Leu Gly Asp Val Gln Gly Val Asn
770 775 780

Asn Lys Glu Arg Ala Ala Leu Gly Asp Asn Val Asp Ile Ser Thr Pro
785 790 795 800

Asn Asp Gly Asp Val
805

<210> 5
<211> 673
<212> DNA
<213> Mus musculus

<220>
<223> CMV promoter sequence

<400> 5
tggccattgc atacgttgta tccatatcat aatatgtaca tttatattgg ctcatgtcca 60
acattaccgc catgttgaca ttgattattg actagttatt aatagtaatc aattacgggg 120
tcattagttc atagcccata tatggagttc cgcattacat aacttacggt aaatggcccg 180
cctggctgac cgcccaacga cccccgcca ttgacgtcaa taatgacgta tgttcccata 240
gtaacgccaa tagggacttt ccattgacgt caatgggtgg agtatttacg gttaaactgcc 300
cacttggcag tacatcaagt gtatcatatg ccaagtacgc cccctattga cgtcaatgac 360
ggtaaattggc ccgcctggca ttatgccag tacatgacct tatgggactt tcctacttgg 420
cagtacatct acgtattagt catcgctatt accatggtga tgcgggttttg gcagtacatc 480
aatgggctg gatagcgggt tgactcacgg ggatttccaa gtctccaccc cattgacgtc 540
aatgggagtt tgttttggca ccaaaatcaa cgggactttc caaatgtcg taacaactcc 600
gccccattga cgcaaatggg cggtaggcgt gtacgggtgg aggtctatat aagcagagct 660
cgtttagtga acc 673

<210> 6
 <211> 655
 <212> DNA
 <213> Mus musculus

<220>
 <223> CA1 promoter sequence (without the R region and with two bases deletion in the promoter region in addition thereto)

<400> 6
 attgattatt gactagttat taatagtaat caattacggg gtcattagtt catagcccat 60
 atatggagtt ccgcgttaca taacttacgg taaatggccc gcctggctga ccgccaacg 120
 acccccgccc attgacgtca ataatgacgt atgttcccat agtaacgcca atagggactt 180
 tccattgacg tcaatgggtg gactatttac ggtaaactgc ccacttggca gtacatcaag 240
 tgtatcatat gccaagtacg cccctattg acgtcaatga cggtaaattg cccgcctggc 300
 attatgcca gtacatgacc ttatgggact ttcctacttg gcagtacatc tacgtattag 360
 tcatcgctat taccatgggt cgaggtgagc cccacgttct gcttcactct ccccatctcc 420
 cccccctccc ccccccaat tttgtattta tttatttttt aattattttg tgcagcgatg 480
 ggggcggggg gggggggggc gcgcgccagg cggggcgggg cggggcgagg ggcggggcgg 540
 ggcgaggcgg agaggtgcgg cggcagccaa tcagagcggc gcgctccgaa agtttccttt 600
 tatggcgagg cggcggcggc ggcggcccta taaaagcga agcgcgcggc gggcg 655

<210> 7
 <211> 657
 <212> DNA
 <213> Mus musculus

<220>
 <223> CA2 promoter sequence (without the R region)

<400> 7
 attgattatt gactagttat taatagtaat caattacggg gtcattagtt catagcccat 60
 atatggagtt ccgcgttaca taacttacgg taaatggccc gcctggctga ccgccaacg 120
 acccccgccc attgacgtca ataatgacgt atgttcccat agtaacgcca atagggactt 180
 tccattgacg tcaatgggtg gactatttac ggtaaactgc ccacttggca gtacatcaag 240
 tgtatcatat gccaagtacg cccctattg acgtcaatga cggtaaattg cccgcctggc 300
 attatgcca gtacatgacc ttatgggact ttcctacttg gcagtacatc tacgtattag 360
 tcatcgctat taccatgggt cgaggtgagc cccacgttct gcttcactct ccccatctcc 420
 cccccctccc ccccccaat tttgtattta tttatttttt aattattttg tgcagcgatg 480
 ggggcggggg gggggggggc gcgcgccagg cggggcgggg cggggcgagg ggcggggcgg 540
 ggcgaggcgg agaggtgcgg cggcagccaa tcagagcggc gcgctccgaa agtttccttt 600

tatggcgagg cggcggcggc ggcggcccta taaaaagcga agcgcgcggc gggcggg 657

<210> 8
 <211> 278
 <212> DNA
 <213> Gallus gallus

<220>
 <223> avian beta-actin promoter sequence

<400> 8
 tcgaggtgag cccacgttc tgcttcactc tcccatctc cccccctcc ccaccccaa 60
 ttttgtatit atttatitit taattatitit gtgcagcgat gggggcgggg gggggggggg 120
 cgcgcgccag gcggggcggg gcggggcgag gggcggggcg gggcgaggcg gagaggtgcg 180
 gcggcagcca atcagagcgg cgcgctccga aagtttcctt ttatggcgag gcggcggcgg 240
 cggcggccct ataaaaagcg aagcgcgcgg cgggcggg 278

<210> 9
 <211> 41
 <212> DNA
 <213> Mus musculus

<220>
 <223> forward primer sequence for isolation of the IAP element used
 in Example 1

<400> 9
 gcagcggcgg ccgtggtggc acacactitit agtccccgca g 41

<210> 10
 <211> 41
 <212> DNA
 <213> Mus musculus

<220>
 <223> reverse primer sequence for isolation of the IAP element used
 in Example 1

<400> 10
 ggcgcactag tgatgccctc tcaggcctcc actcaggcac t 41

<210> 11
 <211> 30
 <212> DNA
 <213> Mus musculus

<220>
 <223> forward primer sequence for isolation of the full length of the IAP
 element used in Example 1

<400> 11
 atgcccagat ttcttccacg gctattaggg 30

<210> 12
 <211> 30
 <212> DNA
 <213> Mus musculus

 <220>
 <223> reverse primer sequence for isolation of the full length of the IAP
 element used in Example 1

 <400> 12
 gatgccctct caggcctcca ctcaggcact 30

 <210> 13
 <211> 40
 <212> DNA
 <213> Mus musculus

 <220>
 <223> forward primer sequence related to the CMV promoter used
 in Example 1 (c)

 <400> 13
 ccaagcggcc gctggccatt gcatacgttg tatccatatac 40

 <210> 14
 <211> 40
 <212> DNA
 <213> Mus musculus

 <220>
 <223> reverse primer sequence related to the CMV promoter used
 in Example 1 (c)

 <400> 14
 gcgagaaaaa cggttcacta aacgagctct gcttatatag 40

 <210> 15
 <211> 30
 <212> DNA
 <213> Mus musculus

 <220>
 <223> forward primer sequence related to the R region of the IAP used
 in Example 1 (c)

 <400> 15
 ttagtgaacc gtttttctcg ctctcttgct 30

 <210> 16
 <211> 30
 <212> DNA
 <213> Mus musculus

 <220>
 <223> reverse primer sequence related to the R region of the IAP used

in Example 1 (c)

<400> 16
tctgaaatga agtatccctc ctgcgccagt 30

<210> 17
<211> 63
<212> DNA
<213> Mus musculus

<220>
<223> a linking sequence of a linker DNA used in Example 3

<400> 17
cgaatcgtaa ccgttcgtac gagaattcgt acgagaatcg ctgtcctctc caacgagcca 60
agg 63

<210> 18
<211> 26
<212> DNA
<213> Mus musculus

<220>
<223> a linking sequence of a linker DNA used in Example 3

<400> 18
ccttggtcgtc tttttttttg caaaaa 26

<210> 19
<211> 25
<212> DNA
<213> Mus musculus

<220>
<223> a linker specific primer for use in the first round
in Example 3 (forward)

<400> 19
cgaatcgtaa ccgttcgtac gagaa 25

<210> 20
<211> 30
<212> DNA
<213> Mus musculus

<220>
<223> a linker specific primer for use in the first round
in Example 3 (reverse)

<400> 20
gagatgcatg ctttgcatac ttctgcctgc 30

<210> 21
<211> 25
<212> DNA

<213> Mus musculus

<220>

<223> a linker specific primer for use in the second round
in Example 3 (forward)

<400> 21

tcgtacgaga atcgctgtcc tctcc

25

<210> 22

<211> 30

<212> DNA

<213> Mus musculus

<220>

<223> a linking sequence of neo cassette specific primer for use
in the second round in Example 3 (reverse)

<400> 22

ggagcctggg gactttccac acctggttgc

30

<210> 23

<211> 30

<212> DNA

<213> Mus musculus

<220>

<223> an alternative linking sequence of neo cassette specific primer
for use in the second round in Example 3 (reverse)

<400> 23

ggggagcctg gggactttcc acaccctaac

30

<210> 24

<211> 39

<212> DNA

<213> Gallus gallus

<220>

<223> a primer 5' upstream until the transcription initiation site of
chicken beta-actin promoter used in Example 4

<400> 24

gcaatgcggc cgcattgatt attgactagt tattaatag

39

<210> 25

<211> 39

<212> DNA

<213> Gallus gallus

<220>

<223> a primer 3' of chicken beta-actin promoter used in Example 4

<400> 25

cgagaaaaac cgcccggcgc gcgcttcgct ttttatagg

39

<210> 26
 <211> 40
 <212> DNA
 <213> Gallus gallus

<220>
 <223> an alternative primer 3' of chicken beta-actin promoter used
 in Example 4

<400> 26
 cgagaaaaac cccgccgcc gcgcgcttcg ctttttatag 40

<210> 27
 <211> 36
 <212> DNA
 <213> Mus musculus

<220>
 <223> a primer of the 5' upstream from the 5' terminus of the R region of
 the IAP to the downstream of the U5 region used in Example 4

<400> 27
 cgcggcgggc gggttttctc gctctcttgc ttcttg 36

<210> 28
 <211> 30
 <212> DNA
 <213> Mus musculus

<220>
 <223> a primer of the 3' side from the 5' terminus of the R region of the IAP
 to the downstream of the U5 region used in Example 4

<400> 28
 tctgaaatga agtatccctc ctgcgccagt 30

<210> 29
 <211> 36
 <212> DNA
 <213> Mus musculus

<220>
 <223> an alternative primer of the 3' side from the 5' terminus of
 the R region of the IAP to the downstream of the U5 region used
 in Example 4

<400> 29
 cggcgggcgg gggttttctc gctctcttgc ttcttg 36

<210> 30
 <211> 903
 <212> DNA
 <213> Mus musculus

<220>
 <223> gamma globin intron sequence

<400> 30
 gtgagtccag gagatgtttc agcactgttg cctttagtct cgaggcaact tagacaactg 60
 agtattgac tgagcacagc aggggtgtgag ctgtttgaag atactggggt tgggggtgaa 120
 gaaactgcag aggactaact gggctgagac ccagtggcaa tgttttaggg cctaaggaat 180
 gcctctgaaa atctagatgg acaactttga ctttgagaaa agagaggtgg aaatgaggaa 240
 aatgactttt ctttattaga tttcggtaga aagaactttc acctttcccc tatttttgtt 300
 attcgtttta aaacatctat ctggaggcag gacaagtatg gtcgttaaaa agatgcaggc 360
 agaaggcata tattggctca gtcaaagtgg gggaactttg gtggccaaac atacattgct 420
 aaggctattc ctatatcagc tggacacata taaaatgctg ctaatgcttc attacaaact 480
 tatatccttt aattccagat gggggcaaag tatgtccagg ggtgaggaac aattgaaaca 540
 tttgggctgg agtagatttt gaaagtcagc tctgtgtgtg tgtgtgtgtg tgtgtgtgtg 600
 tgtgtgtgcg cgcacgtgtg tttgtgtgtg tgtgagagcg tgtgtttctt ttaacgtttt 660
 cagcctacag catacagggt tcatgggtggc aagaagataa caagatttaa attatggcca 720
 gtgactagtg ctgcaagaag aacaactacc tgcatttaat gggaaagcaa aatctcaggc 780
 tttgagggaa gttaacatag gcttgattct ggggtggaagc tgggtgtgta gttatctgga 840
 ggccaggctg gagctctcag ctactatgg gttcatcttt attgtctcct ttcactctca 900
 cag 903

<210> 31
 <211> 15
 <212> DNA
 <213> Mus musculus

<220>
 <223> a sequence of the tRNA binding site of the full length IAP

<400> 31
 tccgggacga gaaaa 15

<210> 32
 <211> 15
 <212> DNA
 <213> Mus musculus

<220>
 <223> a repeat sequence of the R region of the full length IAP

<400> 32
 ttgcttcttg ctctc 15

<210> 33
 <211> 17
 <212> DNA

<213> Mus musculus

<220>

<223> a specific sequence for the full length IAP (tRNA binding site)

<400> 33

tggtgccgaa ttccggg

17

<210> 34

<211> 15

<212> DNA

<213> Mus musculus

<220>

<223> a tandem repeat sequence specific for the full length IAP

<400> 34

aatccgggac gagaa

15

<210> 35

<211> 11

<212> DNA

<213> Mus musculus

<220>

<223> a repeat sequence of the R region found in the full length IAP

<400> 35

ttgcttcttg c

11

<210> 36

<211> 378

<212> DNA

<213> Mus musculus

<220>

<223> cytomegalovirus (CMV) enhancer sequence

<400> 36

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accccgccc attgacgtca ataatgacgt atgttcccat agtaacgcca atagggactt 180

tccattgacg tcaatgggtg gagtatttac ggtaaactgc ccacttggca gtacatcaag 240

tgtatcatat gccaagtacg cccctattg acgtcaatga cggtaaattgg ccgcctggc 300

attatgcca gtacatgacc ttatgggact ttcctacttg gcagtacatc tacgtattag 360

tcacgctat taccatgg 378

<210> 37

<211> 30

<212> DNA

<213> Artificial

<220>
 <223> synthetic sequence in the sense direction of 1st primer used
 in Example 8

<400> 37
 agggctgcgg caagggcaac atcctgttcg 30

<210> 38
 <211> 30
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic sequence in the antisense direction of 1st primer used
 in Example 8

<400> 38
 gccgccgtcc tccacgtagg tcttctccag 30

<210> 39
 <211> 30
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic sequence in the sense direction of 2nd primer used
 in Example 8

<400> 39
 ggcaaccagc tgggtgcagat ccgcgtgacc 30

<210> 40
 <211> 30
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic sequence in the antisense direction of 2nd primer used
 in Example 8

<400> 40
 gtccttcacc acgcccttgc tcttcatcag 30